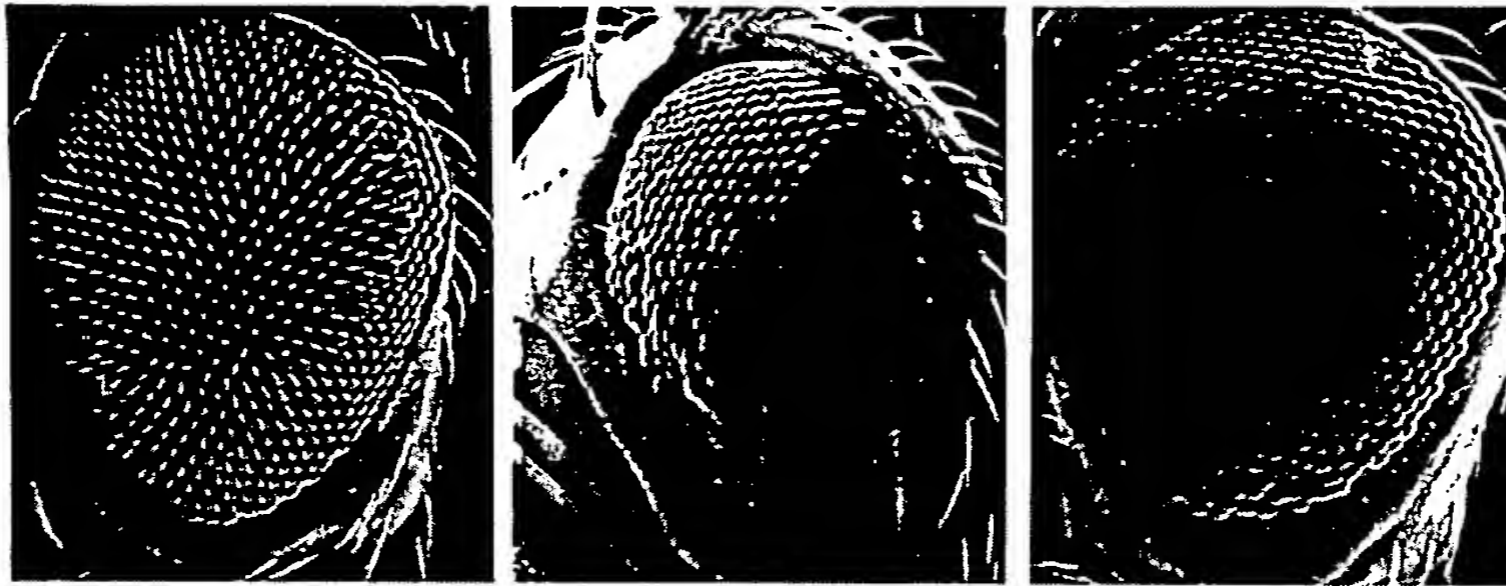


Figure 1

A



wild type

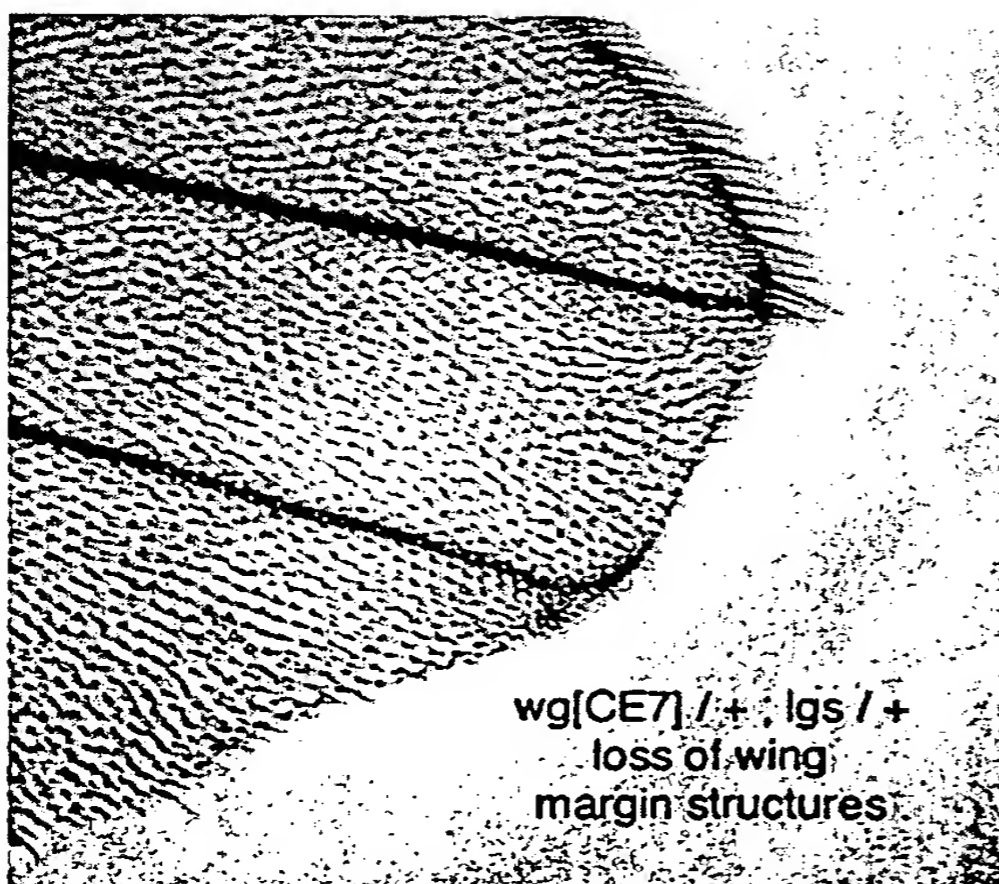
sev-wg

sev-wg, $lgs^{S17}/+$

B



C



wg[CE7]/+ ; lgs/+
 loss of wing
 margin structures



wg[IL114]/+ ; lgs/+
 Janus phenotype (double dorsal)

Figure 2

ACGAGTGCCTCTCTTATTATGCGAGCTGTTTATTCCAAAGTATGTTTCGCAATTTTCGACT	60	GCGCGCCTAGCAACTCTTTTGTGACCGAGTCTGATCCTATGGGCAACGAACTGAATTGA	3060
CCTGCTAACATAACCGCACOGTTAAAGCAGGAACATTTTGGGCTATAAGCCCAAAATTTCA	120	A P S N S F V D Q S D P M G N E T E L M	445
TTAGCTTAATACGATGCTCCGAAAGTGTATTGCAATTTGCAATATACATAAAAAATTGTAC	180	TGTGCTGGGAAGGCGGATCCTCAAAACCCAGTAGGTCTGGACAAAACCTCAGCAATCATG	3120
ATAGAAATAGGAGAAATTCACATACAAATACAAAAATACAAAAATCCTCCAGTAAAAATTTAA	240	C W E G G S S N T S R S G Q N S R N H V	465
AACGATATCGTGTGTTTGTCTTCGCGTATCTCAGTGCAGATGTAATCGCATGCATATGAGTG	300	TAGACAGTATCAGTACATCCAGCGAGTCAACAGGCAATAAAGATACTGGAAAGCAGCTGGCG	3180
GTGAGTGCCTTCGCTGCAGTTCTCGTCTAAATATGCTTAATTGCGTTTCGCGAGCTTCAAA	360	D S I S T S S E S Q A I K I L E A A G V	485
AGCAATAAAACGATOGATTTTTAAATTCGTACTTTGAGCAATTAGCCACACAAGGGATCTTGG	420	TTGATTTGGGACAGGTCAAAAAAGGAAGCGATCCTGGCCTGACAACTGAAAACAACATTG	3240
GAAAGTCGATTTTGAAGAAATTCGATTTCATAGGATGCTCTCGACAACTATGCCCCCAGCTC	480	D L G Q V T K G S D P G L T T E N N I V	505
	5	TATCACTGCAAGGAGTTAAGTTCCAGACGAAAACTTACACCAACACAGCGGCAACATC	3300
CAACCCAAACACAGCCGCAACCAAACTCCGATGCCTCCTCAACAGTGCAATCTGATCAAA	540	S L Q G V K V P D E N L T P Q Q R Q H R	525
T Q Q Q P Q P N S D A S S T S A S G S N	25	GCGAAGAACAGTTGGCAAAAAATAAAAAAATGAATCAATTTCTTTTCTGAAAAAGAGA	3360
ATCCTGGAGCAGCGATCGGAAAATGGGACTCGGCGCGAGCAGAAAGTTCTTCGGAAGACCC	600	E E Q L A K I K K M N Q F L F P E N E N	545
P G A A I G N G D S A D E Q S S K P N K T L	45	ATTCAGTAGGAGCTAATGTAAGCTCAGATACAAAAATTCAGGAGATTTAATGATGG	3420
TTAATAGCGAAACCTTTCTACTTTGTTCGCCCGGTAAAGACTTGTAATTGATTCTCTCTTGT	660	S V G A N V S S Q I T K I P G D L M M G	565
N S E P F S T L S P	55	OGATGTCCGGTGGCGAAGCGGATCTATTATTAATCCGACGATGCGACAACTGCATATGC	3480
CCGGAATTATAACAACTTTCTGTGTTTCCAGATCAAAATAAAATTCAGCCGAGAAGAGGC	720	M S G G G G G S I I N P T M R Q L H M P	585
D Q I K L T P E E G	65	CAOGTAAACGCAAAATCGAGCTCTTATCGGCGCAAGTTCAAGGACTTTGGAAGATGTA	3540
ACTGAGAAAAGCGGACTATCAACTAGTGATTAAGCTGCCACTGGAGGAGCCCCAGGAGT	780	Q N A K S E L L S A T S S G L S E D V M	605
T E K S G L S T S D K A A T G G A P G S	85	TCATCCAGGGGATGTTATATCAGATAGGGTGCCGTAAAGGATGTAATAAATAAATAA	3600
GGAAATAATCTGCCCCGAGGACAAACTATGCTAAGGCAGAACTCTACGAGCACAATCAAC	840	H P G D V I S D M G A V I G C N N N Q K	625
G N N L P E G Q T M L R Q N S T S T I N	105	AAACCAGTGTGCAATGTGGATCTGGAGTAGGTGTTGCTACTGGAACAACTGCAGCTGGAG	3660
TCGTGCTAGTTCGCTTCTCCACAAAATCCAGTGAACACTCGAAATAGCAGCAATGTGTCT	900	T S V G C G S G V G V T G T T A A G V	645
S C L V A S P Q N S S E H S N S S N V S	125	TAAATGTCAATATGCTTGCCTCAAGCTCCGCGCGCCGAAATGGCAATATGATGGAGCT	3720
GCTACAGTGGCCCTTACTCAGATGGTAGATTGTGACGAGCAATCGAAGAAAAACAATGT	960	N V N M H C S S S G A P N G N M M G S S	665
A T V G A L T Q M V D C A D E Q S S K P N K T L	145	CTACOGATATGCTAGCTCGTTTGGCAACACAAAGCTGCAACGTCAATCGGAACCGCCCCAG	3780
AGTGTGAAGGACGAGGAAGCTGCTAAGACTGCCCCACAAATGGTTTAAAAATTTTAAAAATG	1020	T D M L A S F G N T S C N V I G T A P D	685
S V K D E E A	152	ATATGTCTAAGGAAGTTTAAATCAAGATAGCCGAAACCAATTCACATCAAGGGGAGTTG	3840
TATTCGGCTTCACCTTTGTGTAATCAATTAATTTGTTTTTTTTTTGCTATACCTACAAATTT	1080	M S K E V L N Q D S R T H S H Q G V A	705
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TTGGAACCGTAATTAAGCTCATAAAAATATTAATTTCACTCTTGATGGAATGCATATCATAG	1200	Q M E W S K I Q H Q F F E E R L K G G K	725
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ATTGCTGTACTTTTAAAGAAATATATTAATTTTAAAAATTTGCTGAGTGAATGATATAATAG	1320	P R Q T V T V P Q Q Q T P S G S G G	745
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ACTAGACCGGTGTAAAGCTAAATTTTATTTTAAAGCTGTCTTAATATCCATAACCAT	1440	N S L N N Q V R P L Q G P P P P Y H S I	765
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E I S S N K A K G Q A A G G G	167	Q R S A S V P I A T Q S P N P S S P N N	785
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C E T A G S S L T V K E S P T D V L G	187	L S L P S P R T T A A V M G L P T A D N S P	805
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S L V N M K K E E R E N H S P T M S P V	207	S M D G T G S L S G S V P Q A N T S T V	825
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G F G S I G N A Q D N S A T P	222	Q A G T T V T L S A N K N C F Q A D T P	845
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GAACTACTATAGCGATATCTCCCTGCCTTTTAAATTTTATTTTAAATAGGAAATACGAATAT	1800	S P S N Q N R S R N T G S S S V L T H N	865
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ATGGGTGTAAATTTGTAGGAAGTTTTCATTTTAGAAGAAATGTGATTATTTTATTAACCC	2040	G Q S S A	890
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V K I	225	D N M K S R R R P S P Q G Q R L S P V N S L	911
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D E M S M E G C N Q L N P D F I N E S L	265	H M Q S N S N S A L N A Y K M G S T N I	951
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N N P A I S S I L V S G V G P I P G I G	285	Q M E	954
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V G A G T G N L L T A N A N G I S S G S	305	R Q A S A Q G G S V Q F S R R S D N	972
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S N C L D Y M Q Q Q N H I F V F S T Q L	325	I P L N P N S G N R P P N K M T Q N F	992
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A N K G A E S V L S G Q F Q T I I A Y H	345	D P I S S L A Q M S Q Q L T S C V S M	1012
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C T Q P A T K S P L E D F F M K N P L K	365	G S P A G T G G M T M M G G P G P S D I	1032
AGATTAAACAAGTTACAGCGGCACAAATCCGTCGGTATGCCATGGATAGGCAATGGGCGAGG	2880	AATATTGAGCATGGAATAATTTTCGGACTAGATGGATCAGGAATAGATACCATAAATCAA	5220
I N K L Q R H N S V G M P W I G M G Q V	385	N I E H G I I S G L D G S G I D T I N Q	1052
TTGGACTAACCTCTCTAATCTGTAGCCAAAAATAACAACAGCAGCCACATACAAGA	2940	AATAACTGTCAATTCMAATGAATGTCGTAATGAATCAATGGTCCCCGAAATGCTGAATCTT	5280
G L T P P N P V A K I T Q Q Q P H T K T	405	N N C H S M N V V M N S M G P R M L N P	1072
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V G L L K P Q F N Q H E N S K R S T V S	425	K M C V A G A G G P N G P P G F N P N S P N	1092
		GGTGGATTAAAGAGAAATTCATAGGGTCTGGCTGTGGCTCAGCAAACTCTTCAAACTTT	5400
		G G L R E N S I G S G C G S A N S N F	1112
		CAAGGGTGTGTTCCACTGGTGGCAGAAATGATGGGTGAAATGCCAGTCAATTTTGGTTGG	5460
		Q G V V P P G A R M M G R M P V N F G S	1132
		AAATTCATTCGGAATATTCAGGTAAAGGGAGTACCCCAACACCATACATATATGCCA	5520
		N F N P N I Q V K A S T P N T I Q Y M P	1152
		GTAAGGGCAAGAACGCCAAACAATAACAACAATGAGCTAATAATGTCGGAATGCCA	5580
		V R A Q N A N N N N N N N G A N N V R M P	1172
		CCTAGTCTGGAAATTTTTCAGAGGTACGCTAACCTCAAAATGGGTGCTGTAGGCAATGGG	5640
		P S L E F L Q R Y A N P Q M G A V G N G	1192
		TCGCCAATATGCCACCATCAGCCAGCGACCGTACTCTGGAAATGCCAGGATGATGGCG	5700
		S I C P P S A S D G T P G M P G L M A	1212
		GGACCAAGAGCCCGAAGTATGCTAATGAATTTCTCCGAGAGCAACACAGAACAGATC	5760

Figure 2: *legless*

G P G A G G M L M N S S G E Q H Q N K I	1232
ACAAACAAATCCTGGGGCAAGCAAATGGTATTAACTTCTTTTCAGAAATGCAATCAAATGTCT	5820
T N N P G A S N G I N F F Q N C N Q M S	1252
ATTGTTGACGAAGAGGTTGATTACCCGGCCATGACGGATCAATGAATATTGGTCAACCA	5880
I V D E E G G L P G H D G S M N I G Q P	1272
TCTATGATAAGGGGCAATGCGTCCACATGCCATGCCGCCAAATGTAAATGGTGGCGGATG	5940
S M I R G M R P H A M R P N V M G A R M	1292
CCACCCGTTAACAGGCAAAATTCAGTTTGCACAGTCATCGGATGGTATTGACTGTGTCGGG	6000
P P V N R Q I Q F A Q S S D G I D C V G	1312
GATCCGTCAATTTTTCAGTAAACGCTTCTGCAACAGCGCTGGACCAACATGTTTGGAT	6060
D P S S F F T N A S C N S A G P H M F G	1332
TCAGCACAAAGGCCAATCAGCCTAAGACACAAACATAAAGAATACCTAGTGAATG	6120
S A Q Q A N Q P K T Q H I K N I P S G M	1352
TGTCAAAACCAATCGGGACTTGCAGTGGCACAAGGCGAGATCCAACTGCATGGGCAAGGA	6180
C Q N Q S G L A V A Q G Q I Q L H G Q G	1372
CATGCGCAGGGTCAGTCTTTAAATGGACCTACTAAATAATTTAAATGTCAACTGCCGGA	6240
H A Q G Q S L I G P T N N N L M S T A G	1392
AGTGTAGTGTACTAAACGCTGTCTTGCATCAAATTCGTAGGTCCCTCTTCTACGGAC	6300
S V S A T N G V S G I N F V G P S S T D	1412
CTGAAGTATGCCCAACCAATATCATAGTTTTCAGCAGCAGTTATATGCTACCAACACCAGA	6360
L K Y A Q Q Y H S F Q Q Q L Y A T N T R	1432
AGTCAACAACAACAGCATATGCCACCAGCAGCACCAGAGCAACATGATAACAAATGCCCGCG	6420
S Q Q Q Q H M H Q Q H Q S N H I T M P P	1452
AAATTTATCACCAAAATCCAAAGTTCTTTGTCAACAAATAAACTTCTAAATTTTGGCGGCC	6480
N L S P N P T F F V N K *	1465
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GAAGCTTATTTACTTAGGTGTTTTTACAACGGAGAAAAATAAACTTTTGGATATGCAAAATG	6600
ATAACGTTGGAAACAAACATAATTCATTTGCAACTTTTAGAAGTCACGTCGAAGTTAAATG	6660
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GTTATCAGCAGCTATTTTCTGTATTTATTTAATATGTGGGCTGCTCTCTCTGTGTAAAT	6780
GAAATTAATAATATATATAATGTAACCGCTATTGATATATATGCTCTCAACTGTAT	6840
TGTAATCAATATTAAGAGAACTGTAAATTCCTCCATATAAAGGTAATGAAAAAAAAAAAA	6900
AAAAAAAAA	6909

Figure 3

A



yw x lgs anti-sense



yw x lgs sense



B

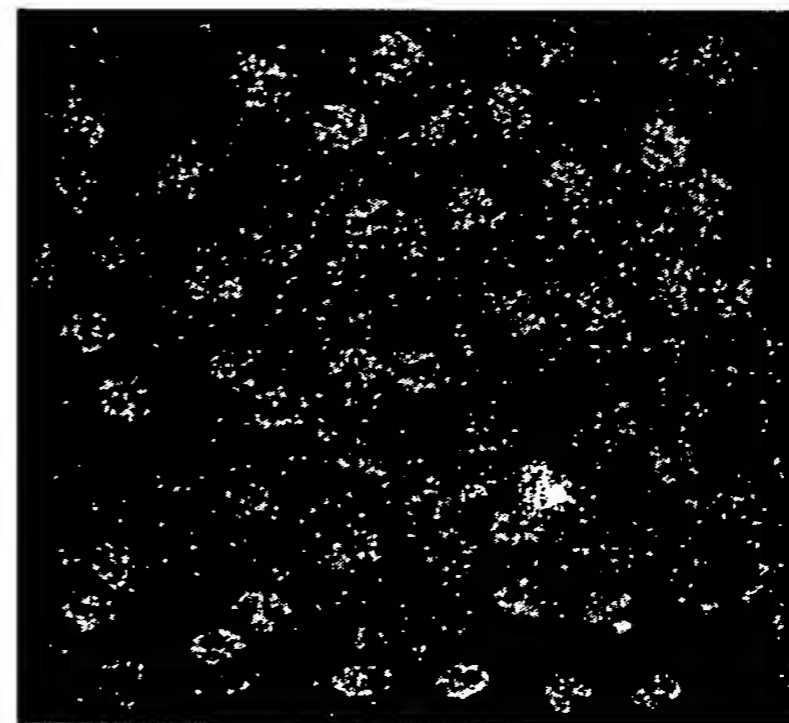
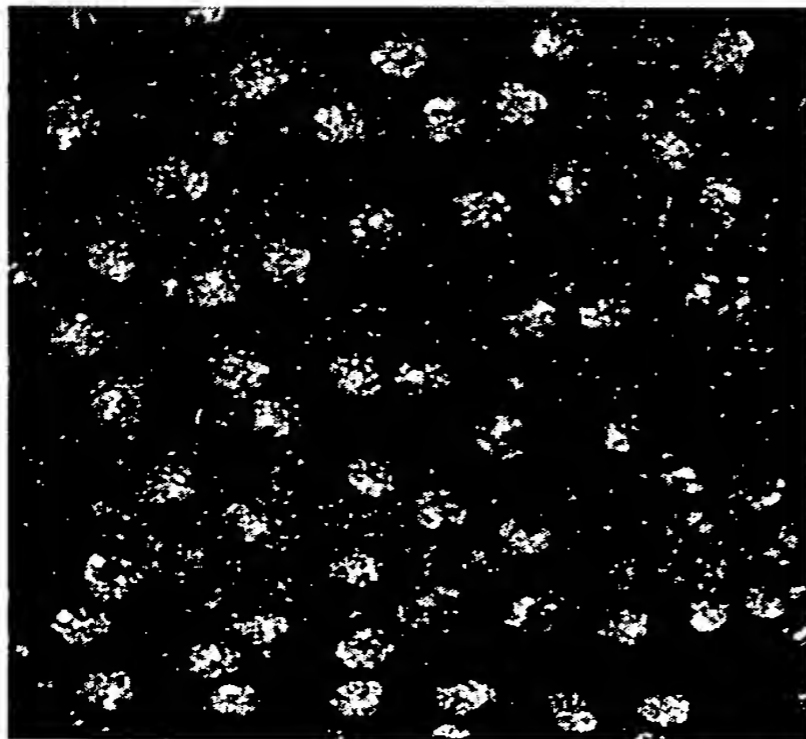


Figure 4

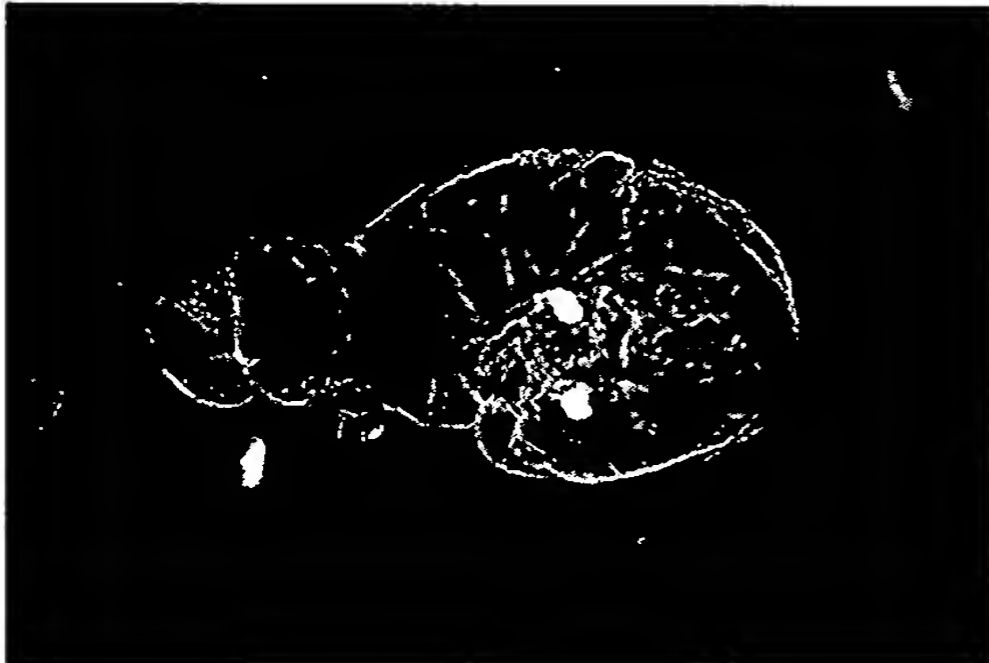
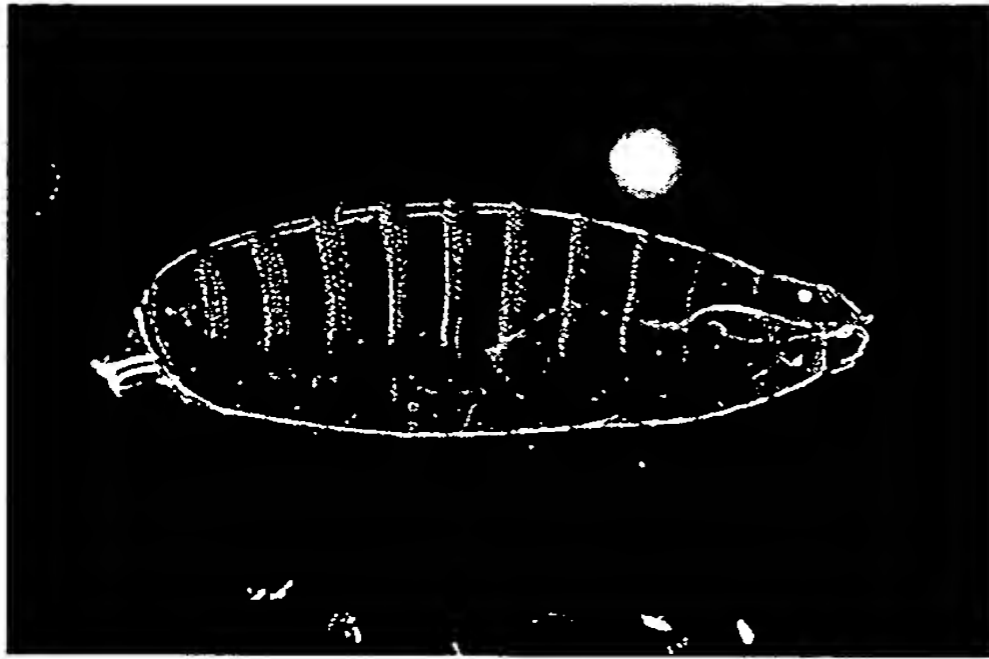
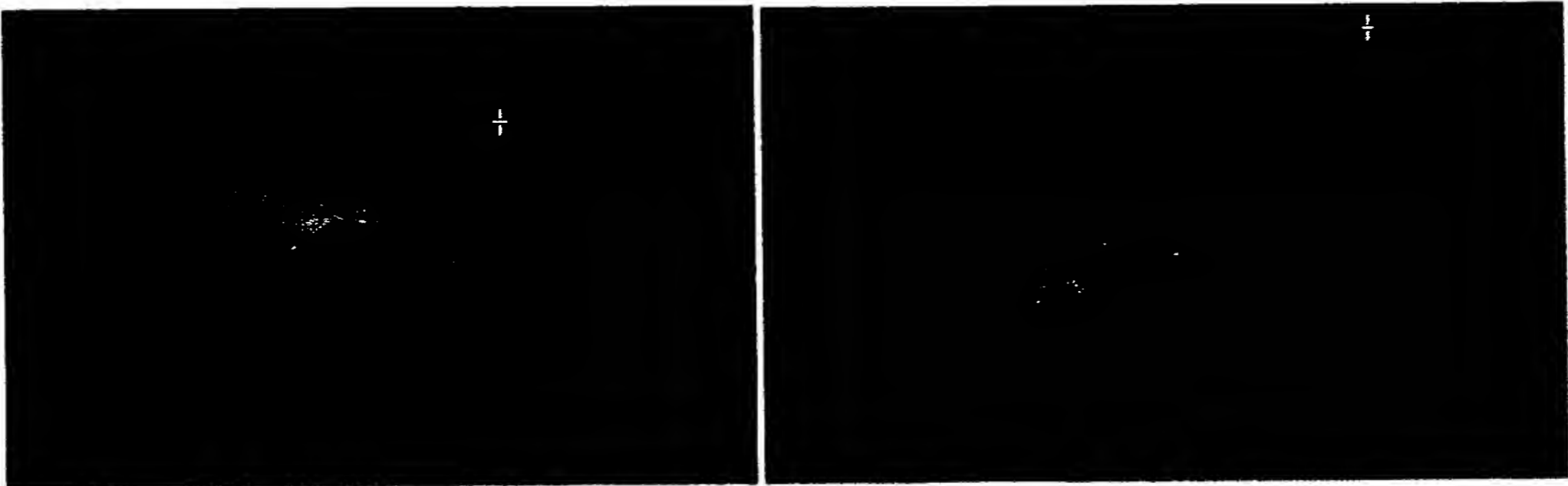


Figure 5

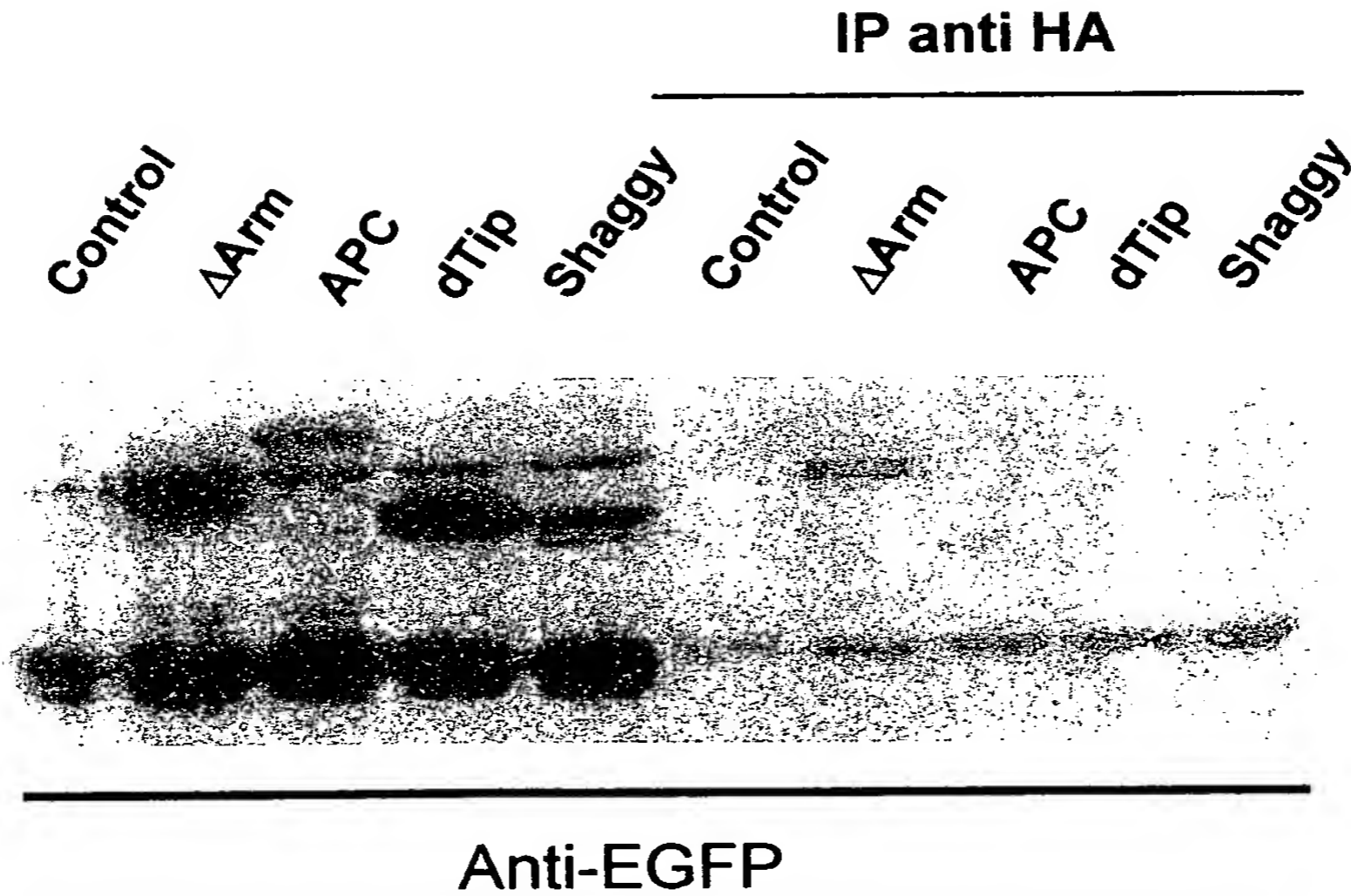
A

EGFP-Lgs

EGFP-Lgs + pcDNA3-Arm-NLS



B

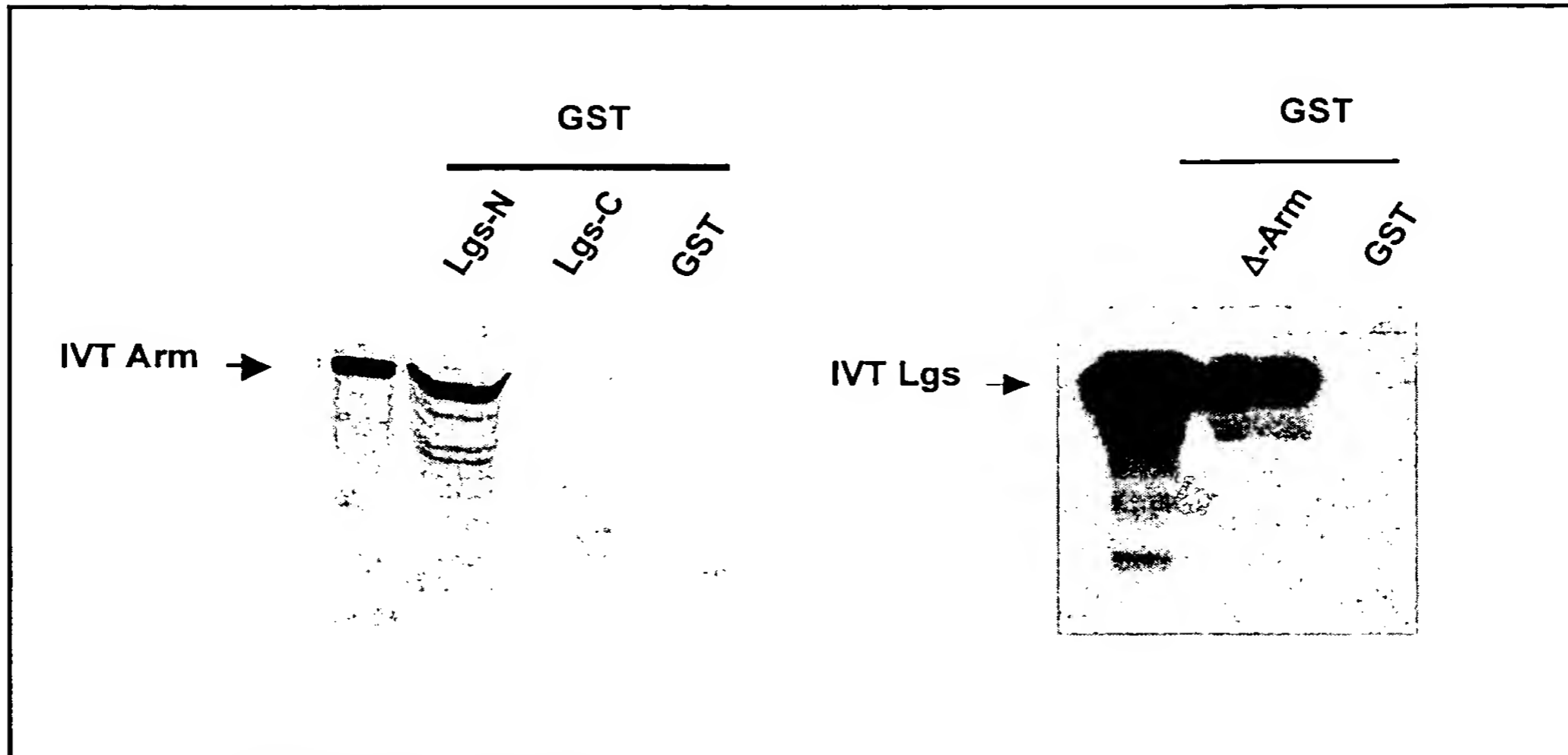


5C

		BAIT fusions: pLex						
		Lgs 1-1464	BCL9 199-392	BCL9 1-1426	Dco+	ΔArmC	Δβ-Cat	Pan
PREY fusions: pJG4-5	lgs364-555					+		
	lgs1-385					-		
	lgs1-732					+		
	lgs364-1090					+		
	lgs726-1464					-		
	lgs1-1464				-	+	n.d.	+
	BCL9 199-392					+	n.d.	
	BCL91-1426					+	+	
	Dco+	-						
	DAxin	(+)				+		
	ΔArmC	+	+	+				+
	β-Cat	+	+	+				
	Pan	+				+		
	pJG4-5	-	-	-		-	-	

+: interaction seen in yeast two-hybrid assay
 -: no interaction seen in yeast two-hybrid assay
 n.d.: not done
 numberings refer to amino acid positions.

5 D



5 E

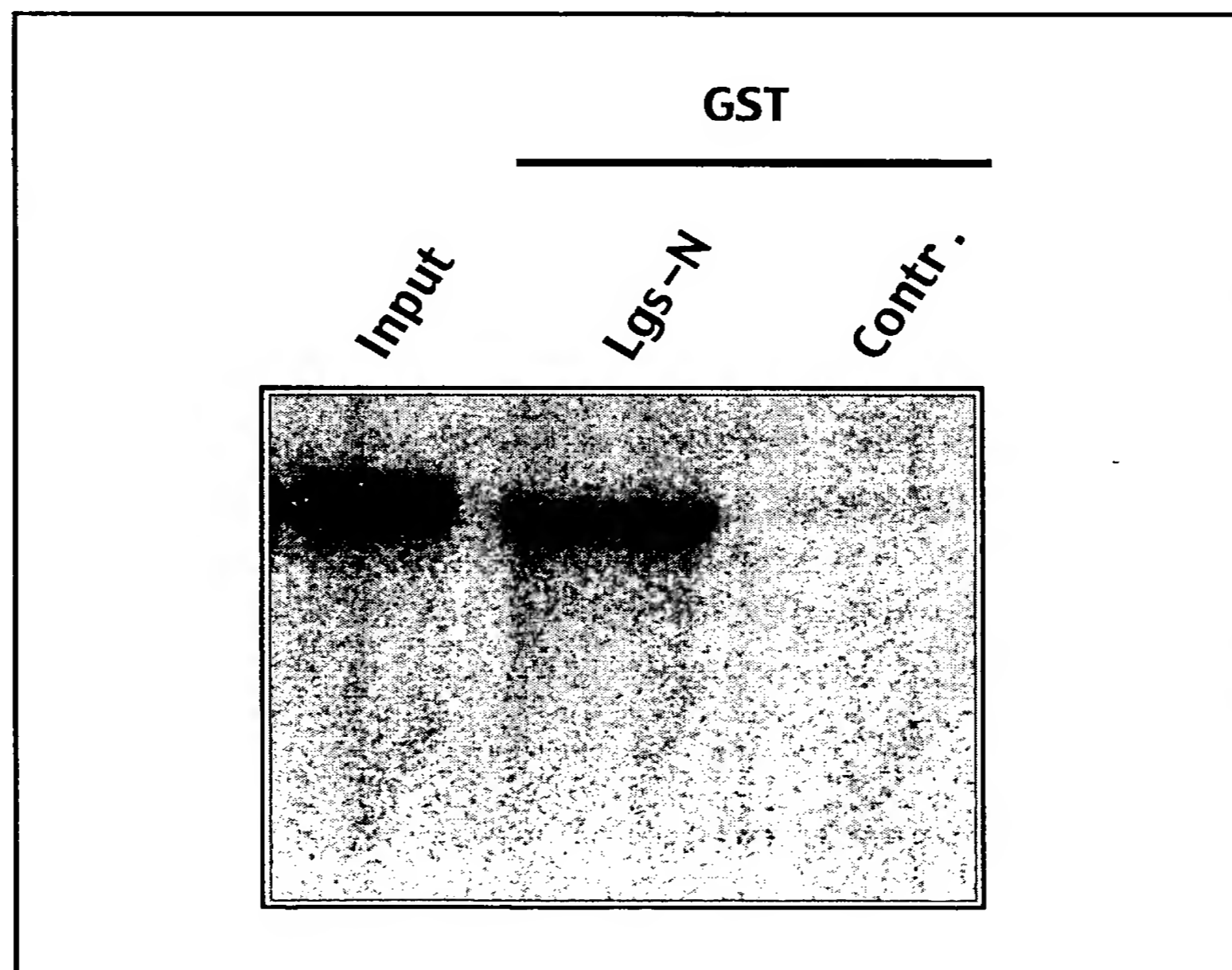


Figure 6

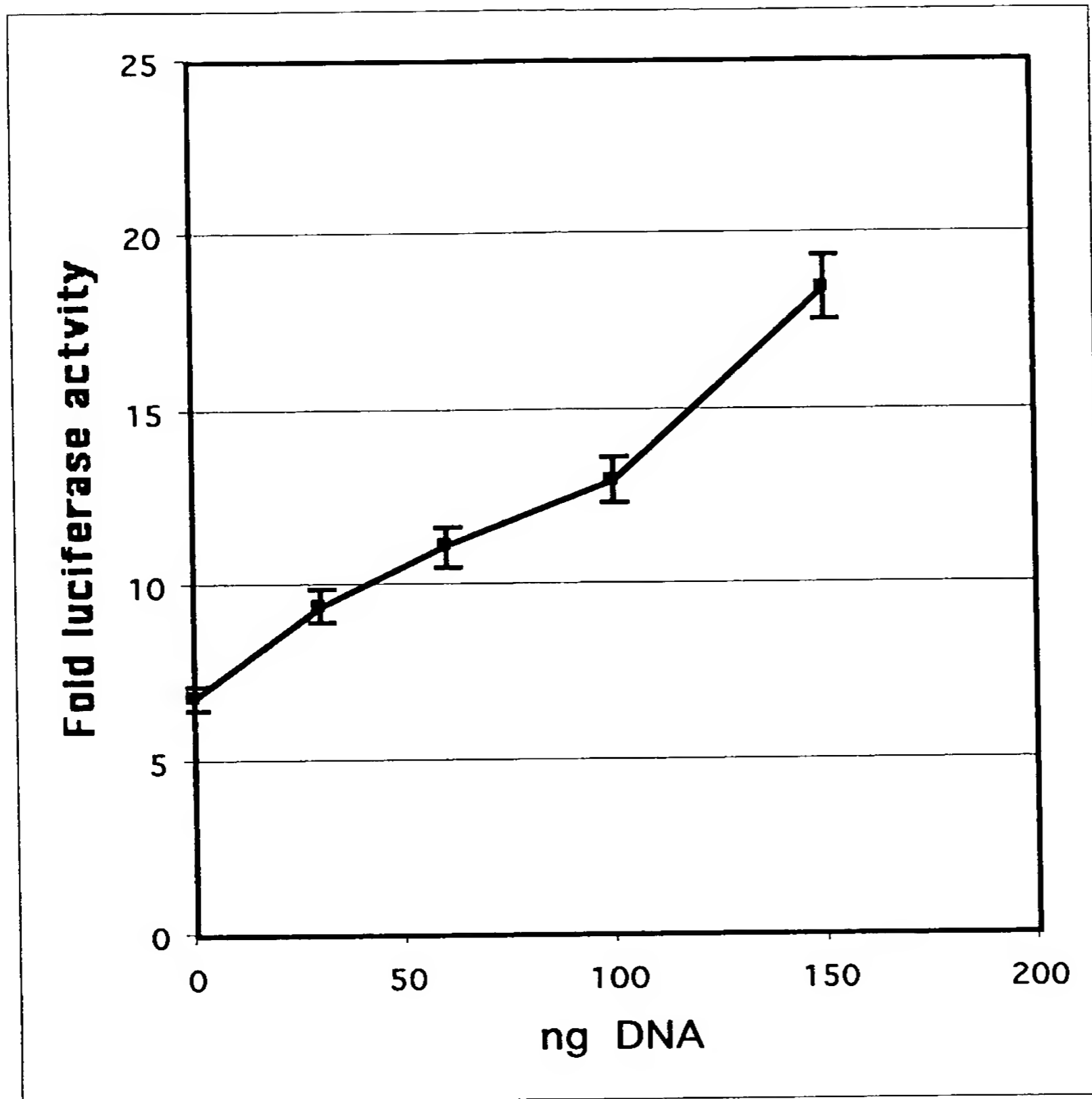
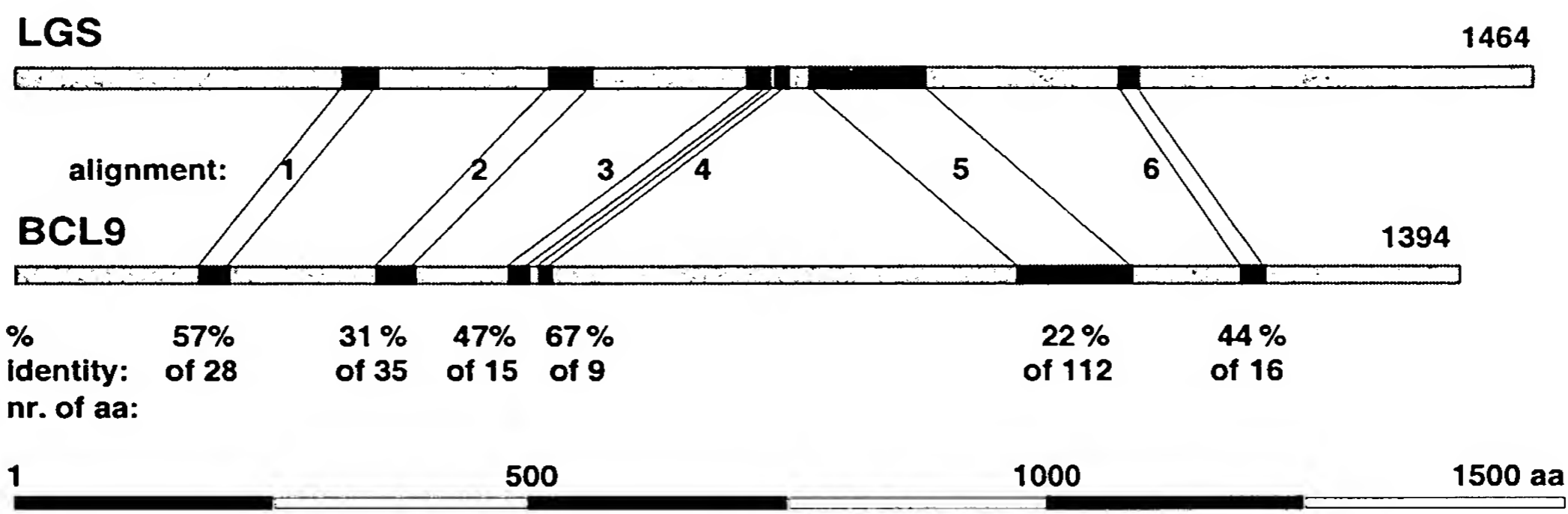


Figure 7

A



7B

Sequence homology domain 1: 57.1% identity in 28 aa

	320	330	340
LGS	IFVFSTQLANKGAESVLSGQFQTIIAYH		
 ::		
BCL9	VYVFSTEMANKAAEAVLKGQVETIVSFH		
	180	190	200

Sequence homology domain 2: 31.4% identity in 35 aa

	520	530	540
LGS	ENLTPQQRQHREEQLAKIKKMNQFLFPENENSVGA		
 :		
BCL9	DGLSQEQLEHRERSLQTLRDIQRMFLFPDEKEFTGA		
	350	360	370 380

Sequence homology domain 3: 46.7% identity in 15 aa

	710	720
LGS	QMEWSKIQHQFFEER	
	
BCL9	QIAWLKLQQEFYEEK	
	470	480

Sequence homology domain 4: 66.6% identity in 9 aa

	760
LGS	LQGPPPPYH

BCL9	VRGPPPPYQ
	520

Sequence homology domain 5: 22.3% identity in 112 aa

	770	780	790	800	810	820
LGS	SASVPIATQSPNPSSPNNLSLPSRPTTAAVMGLPTNSPSMDGTGSLSGSVPQANTSTVQA					
	... :..... :..... : .. : .. : .. : .. : ..					
BCL9	GPPPPTASQPASVNI PGSLPSSTPYTMPPEPTLSQNPLSIM-MSRMSKFAMPSSTPLYHD					
	970	980	990	1000	1010	1020
	830	840	850	860	870	
LGS	GTTTVLSANKNCFQADTPSPSNQNRSRNTGSSSVLTHNLSSNPSTPLSHLSP					
	.. :: : .. : .. : .. : .. : .. : .. : ..					
BCL9	AIKTVASSDDDSPPARSPNLPSPNNMPGNGINTQNPRISGPNFVVPMPPLSP					
	1030	1040	1050	1060	1070	

Sequence homology domain 6: 43.8% identity in 16 aa

	1080
LGS	NPKMCVAGGPNGPPGF
	.. : .. : .. : ..
BCL9	DAALCKPGGPGGPDSE
	1190 1200

Figure 8

A

ATGCATTCCAGTAACCCCTAAAGTGAGGAGCTCTCCATCAGGAAACACACA
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AATACCAGACTGCAGCCAACCTCCACCCATTCCGGCACCAGCACCCAAGCC
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Figure 8A

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Figure 8B

B

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Figure 9

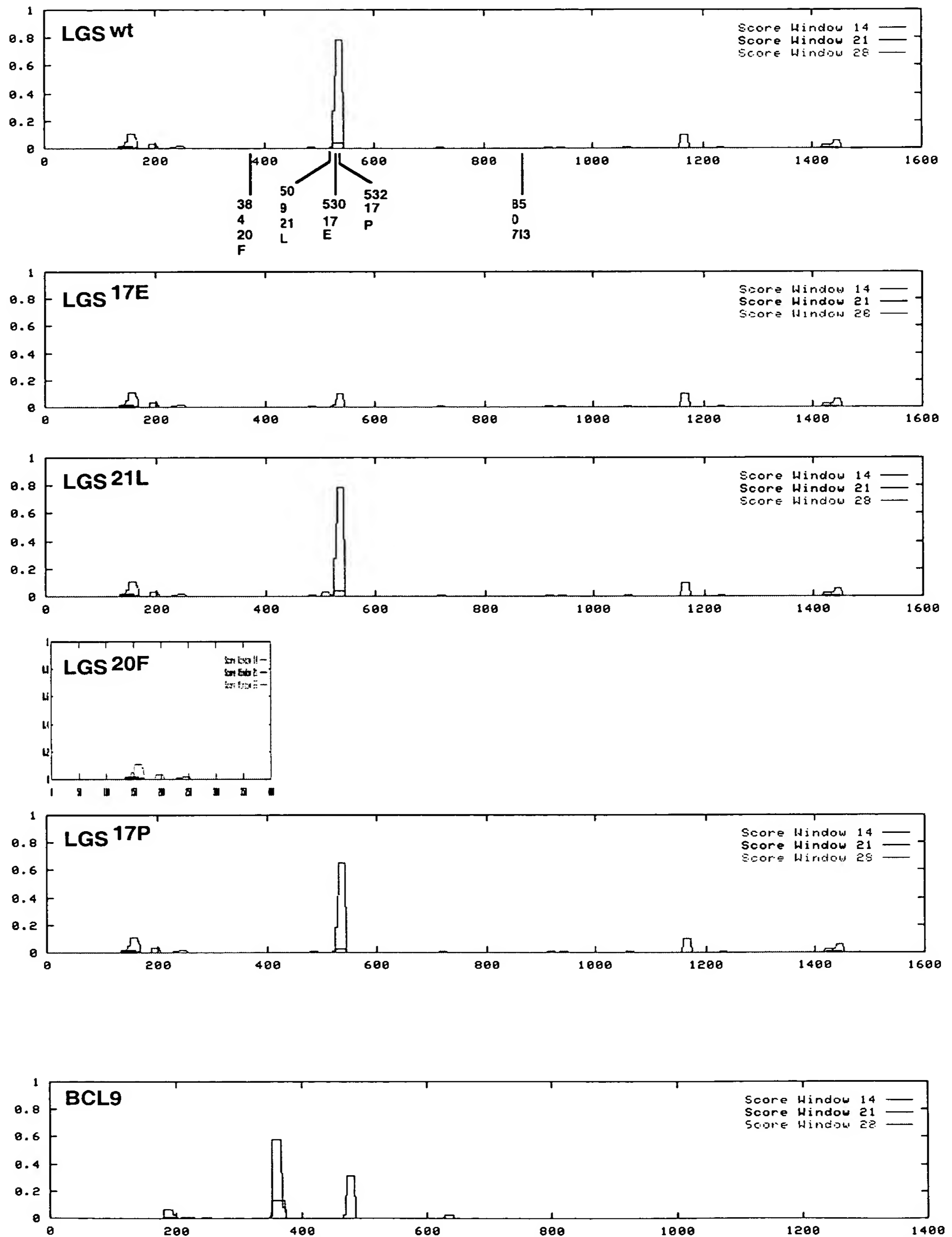


Figure 10

A

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Figure 10

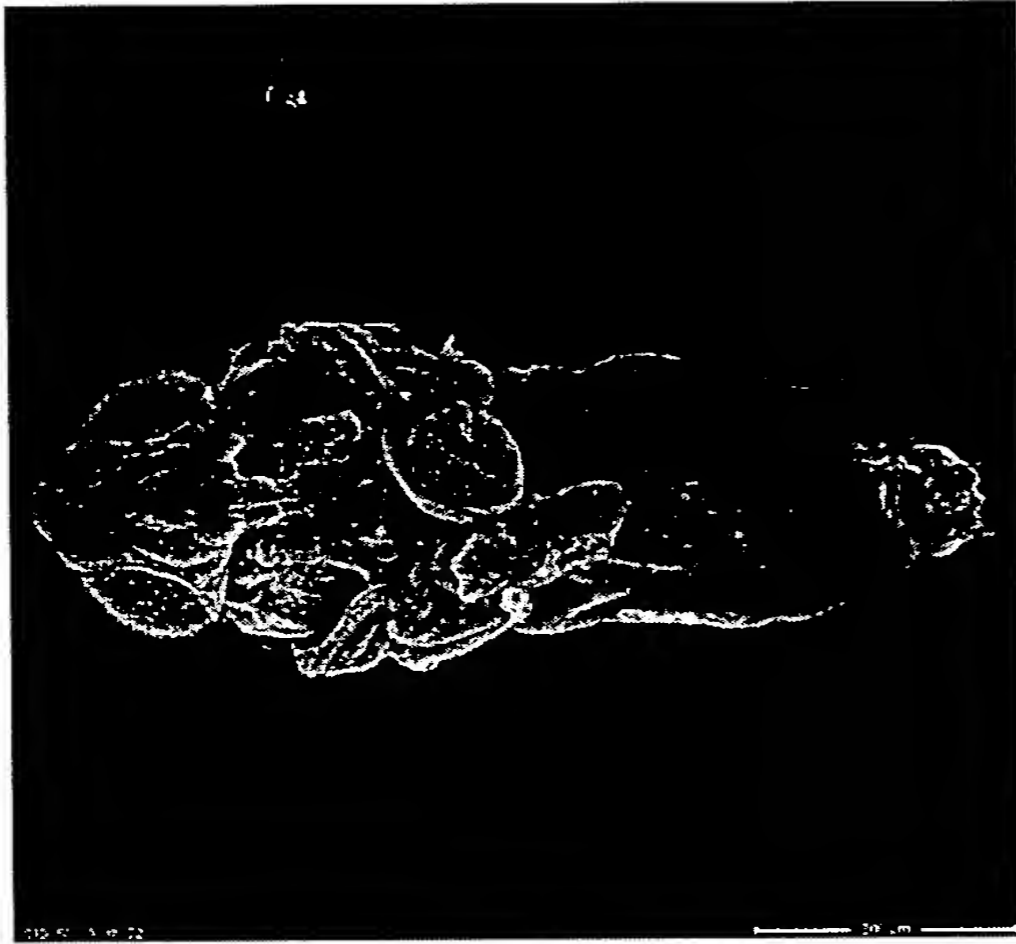
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B

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Figure 11

A



B



Figure 12

A

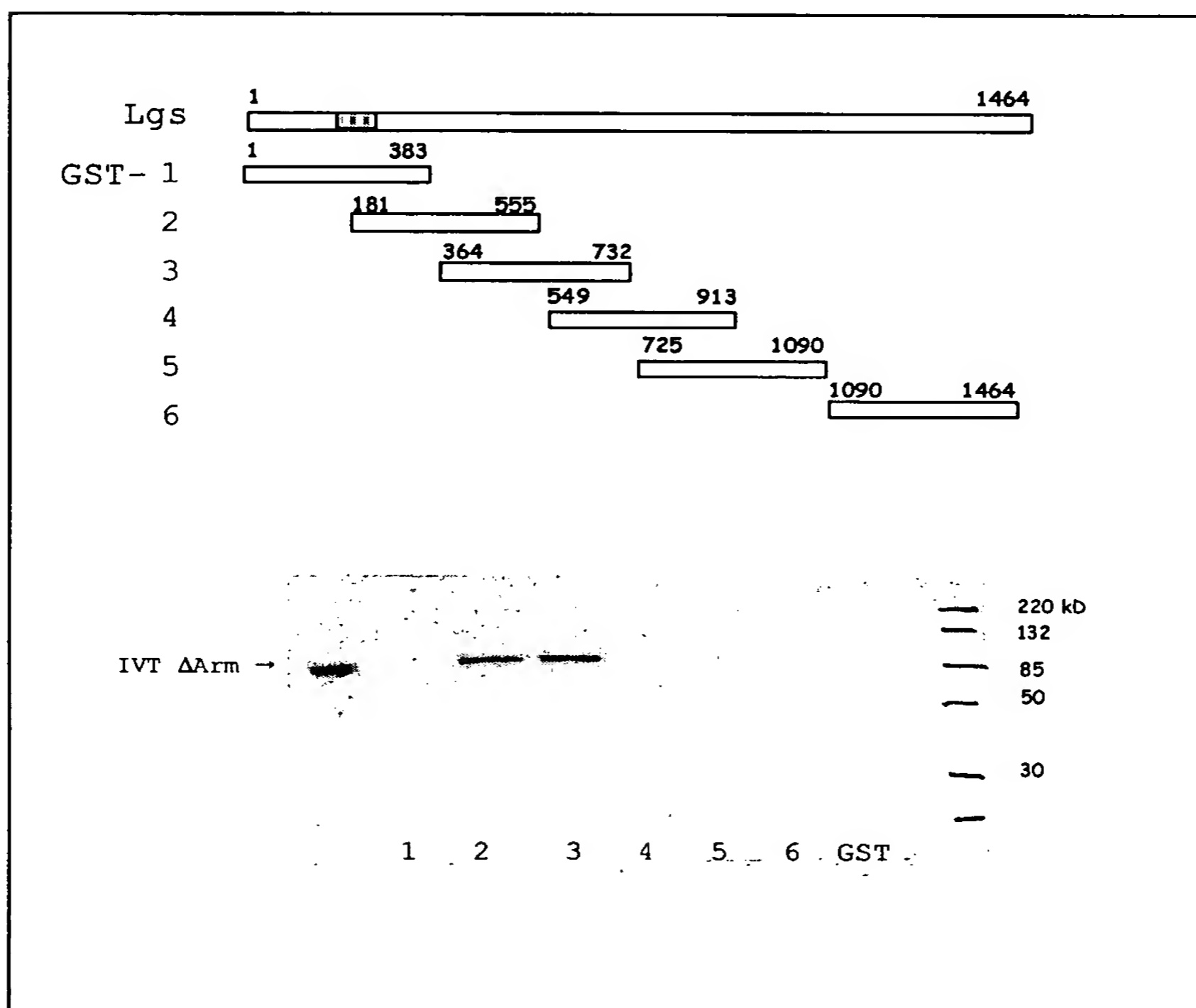
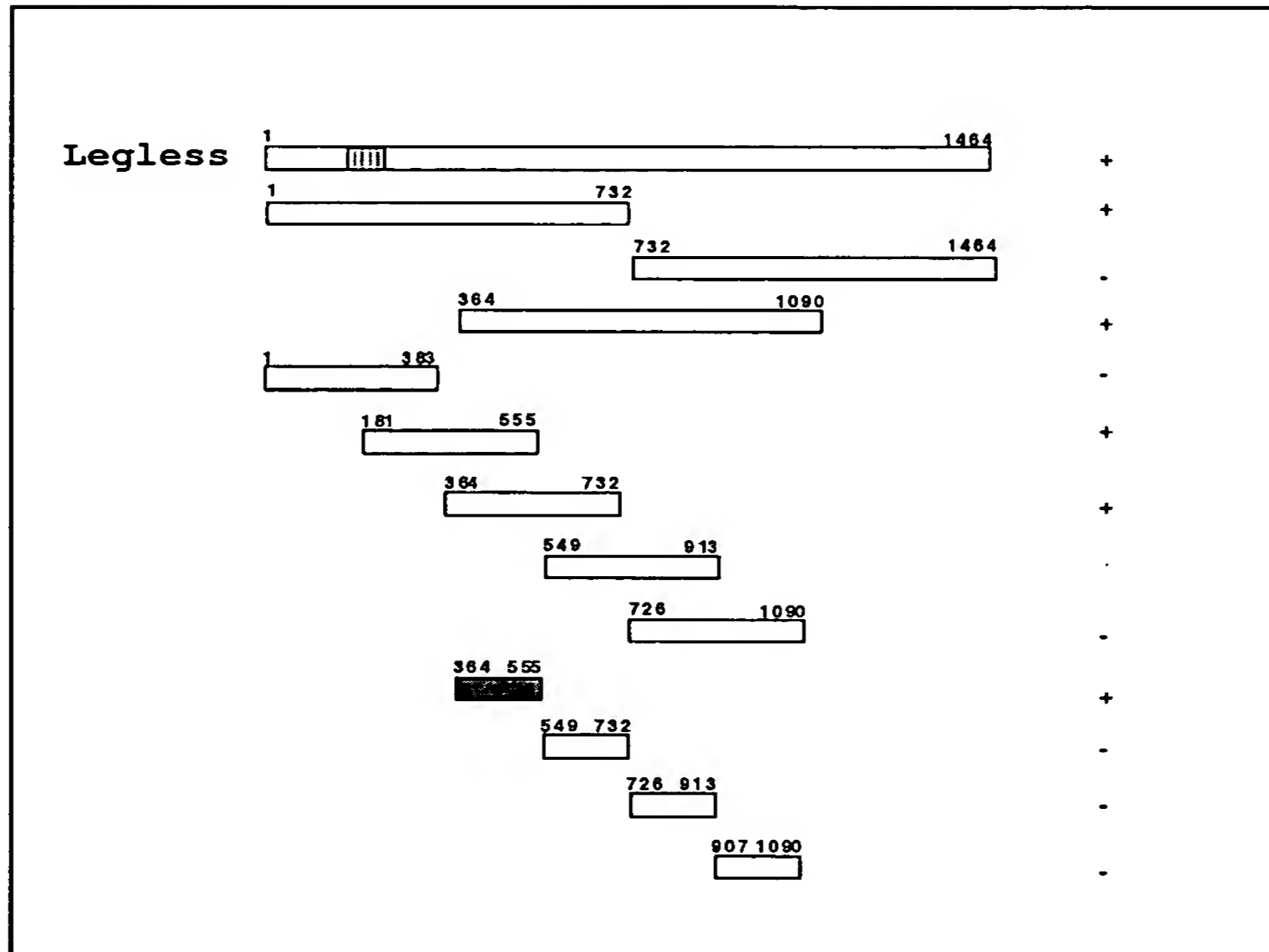


Figure 12B

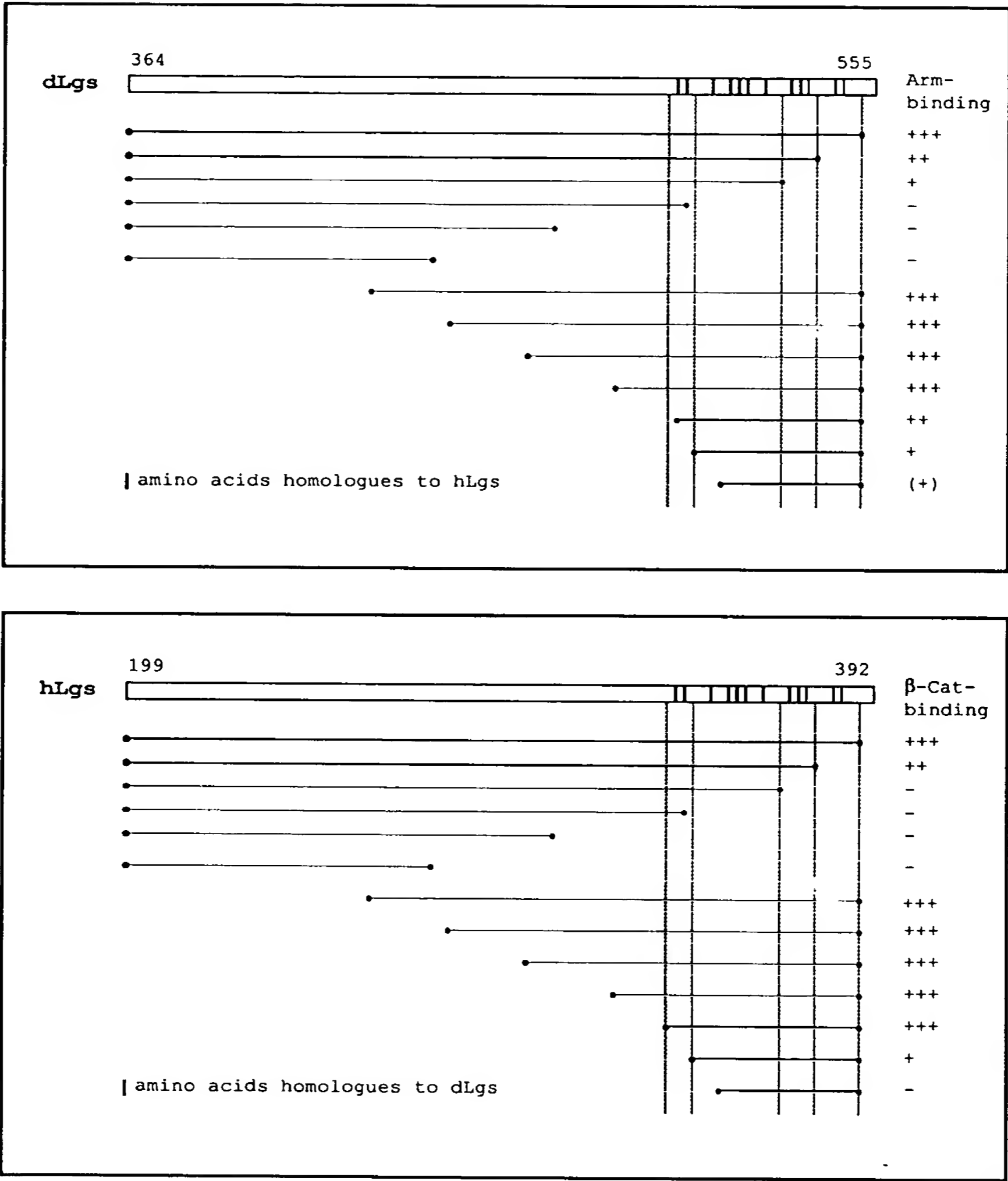


Figure 12C








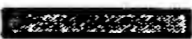

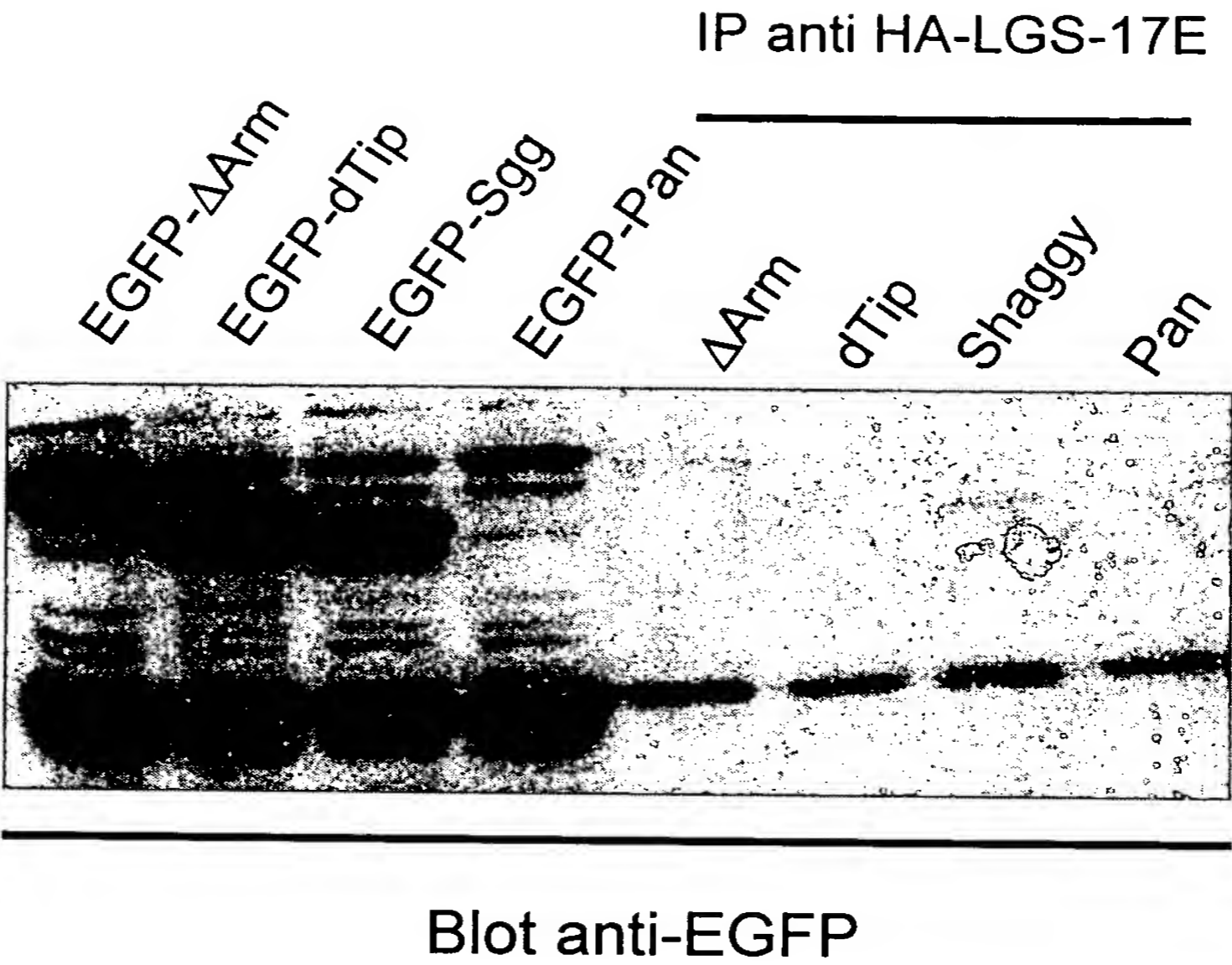
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1 2 3 4 5 6 7 8 9 10 11 12 13  C	++
 C	-
N  1 2 3 4 5 6 7 8 9 10 11 12 13	++
N  1 2 3 4 5 6 7 8	+++
N  1 2 3 4 5 6	+++
N  1 2 3 4	++
N  1 2	-
1 2 3 4 5 6 7 8 9 10 11 12 13	++
1 2 3 4 5 6 7 8	+++
1 2 3 4 5 6	+++
1 2 3 4	++
1 2	-
3 4 5 6 7 8	(+)
5 6 7 8	(-)
7 8 9 10 11 12 13	(-)
9 10 11 12 13	(-)

Figure 13

A

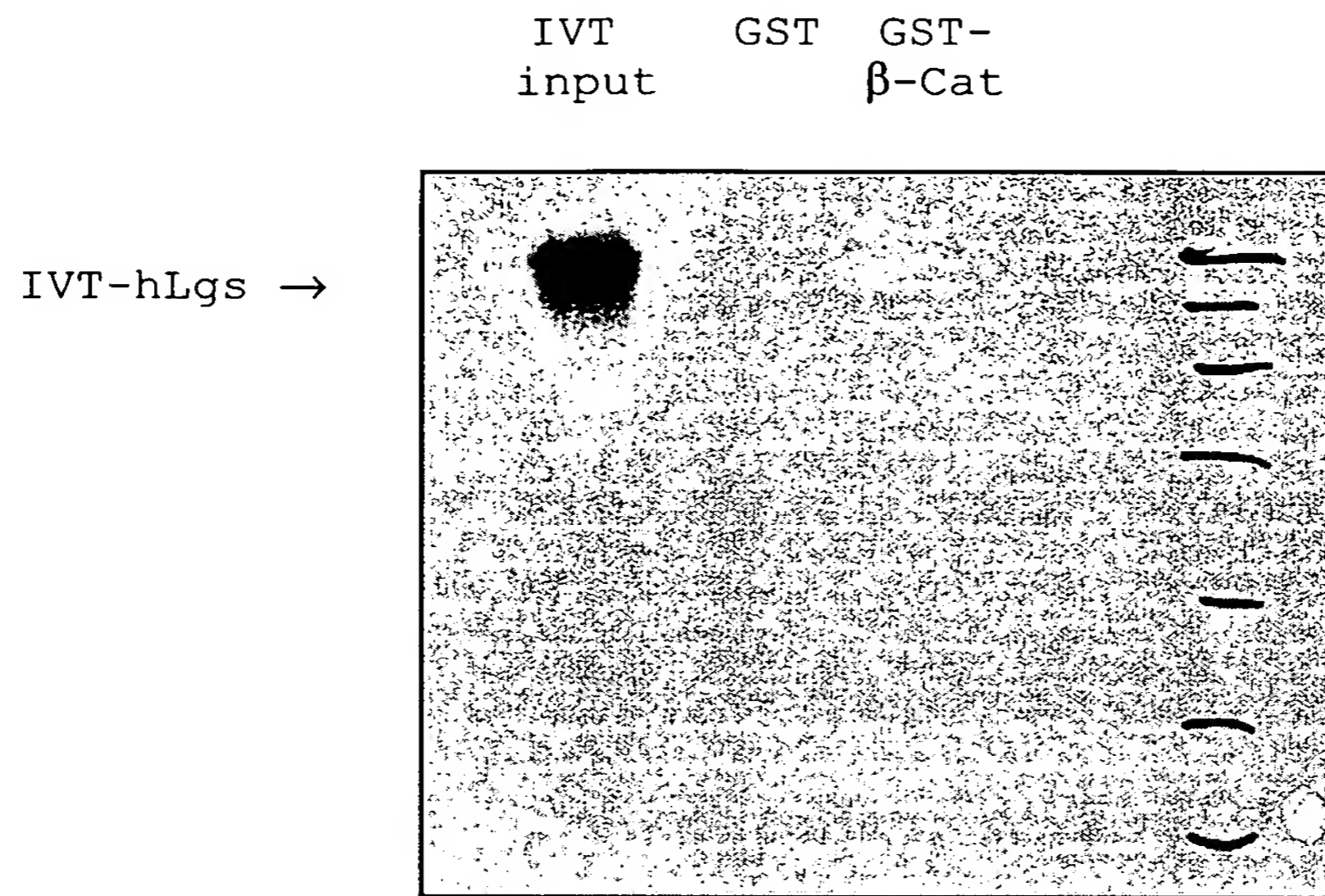


B



Figure 13

C



D

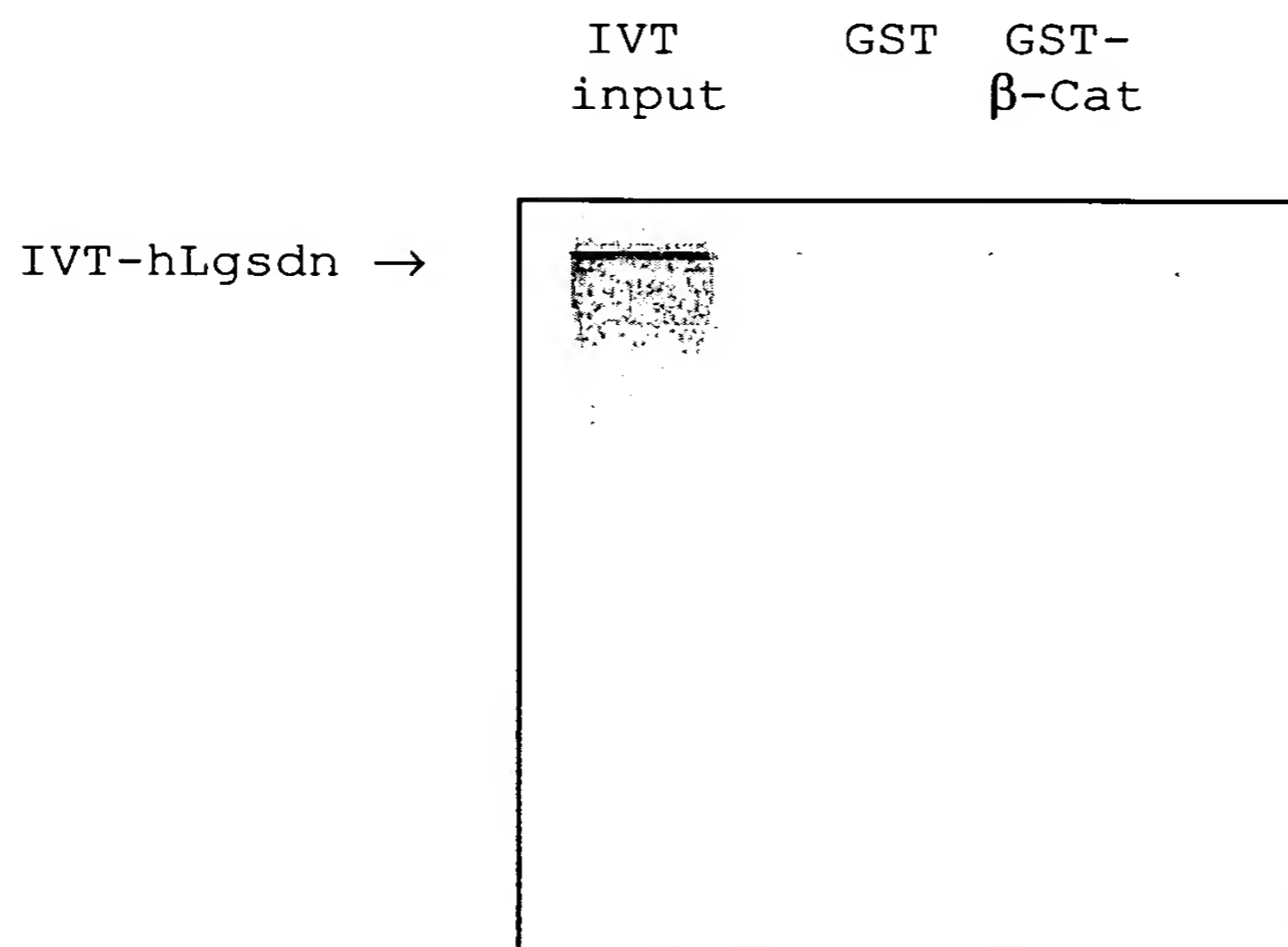


Figure 14

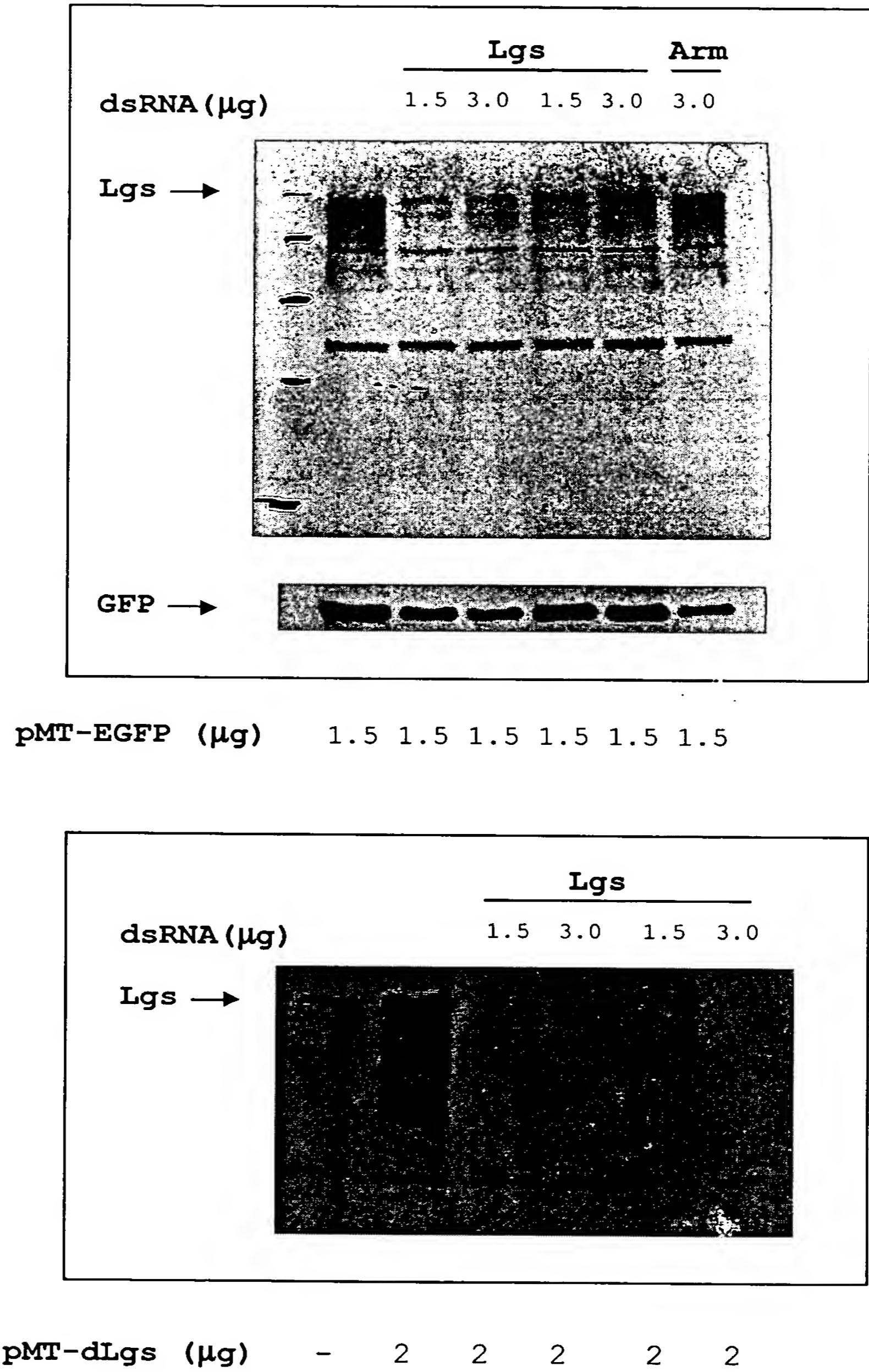
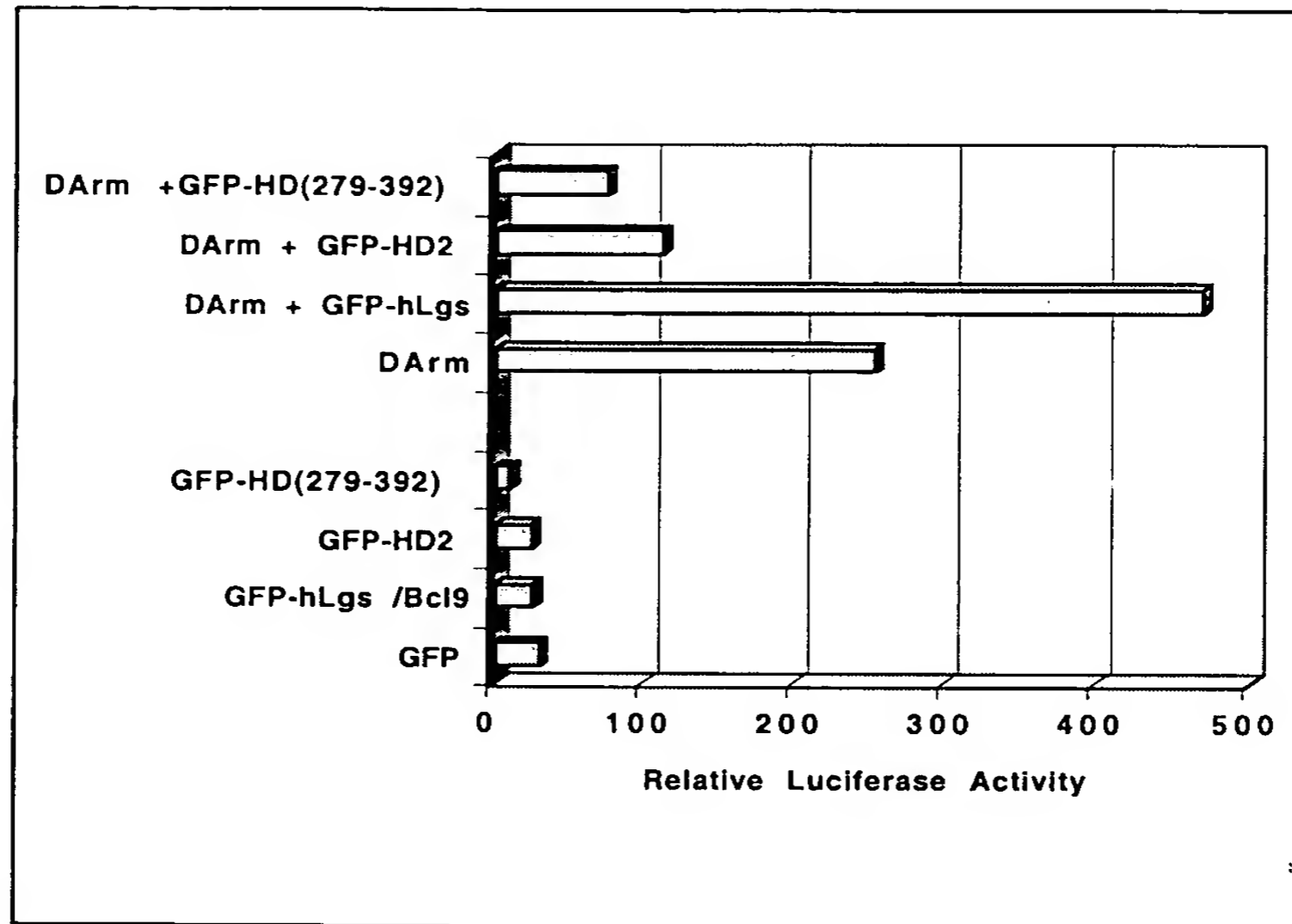


Figure 15

A



B

